Genbank Accession # M21616

Sequence of human PDGF receptor beta

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                          TGTTCTCCTGAGCCTTCAGGAGCCTGCACCAGTCCTGCCTGTCCTTCTACTC    52

AGCTGTTACCCACTCTGGGACCAGCAGTCTTTCTGATAACTGGGAGAGGGCAGTAAGGAGGACTTCC    119

TGGAGGGGGTGACTGTCCAGAGCCTGGAACTGTGCCCACACCAGAAGCCATCAGCAGCAAGGACACC    186

ATG CGG CTT CCG GGT GCG ATG CCA GCT CTG GCC CTC AAA GGC GAG CTG CTG    237
Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu Leu    -15

TTG CTG TCT CTC CTG TTA CTT CTG GAA CCA CAG ATC TCT CAG GGC CTG GTC    288
Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly Leu Val    2

GTC ACA CCC CCG GGG CCA GAG CTT GTC CTC AAT GTC TCC AGC ACC TTC GTT    339
Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser Thr Phe Val    19

CTG ACC TGC TCG GGT TCA GCT CCG GTG GTG TGG GAA CGG ATG TCC CAG GAG    390
Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg Met Ser Gln Glu    36

CCC CCA CAG GAA ATG GCC AAG GCC CAG GAT GGC ACC TTC TCC AGC GTG CTC    441
Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr Phe Ser Ser Val Leu    53

ACA CTG ACC AAC CTC ACT GGG CTA GAC ACG GGA GAA TAC TTT TGC ACC CAC    492
Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly Glu Tyr Phe Cys Thr His    70

AAT GAC TCC CGT GGA CTG GAG ACC GAT GAG CGG AAA CGG CTC TAC ATC TTT    543
Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu Arg Lys Arg Leu Tyr Ile Phe    87

GTG CCA GAT CCC ACC GTG GGC TTC CTC CCT AAT GAT GCC GAG GAA CTA TTC    594
Val Pro Asp Pro Thr Val Gly Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe    104

ATC TTT CTC ACG GAA ATA ACT GAG ATC ACC ATT CCA TGC CGA GTA ACA GAC    645
Ile Phe Leu Thr Glu Ile Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp    121

CCA CAG CTG GTG GTG ACA CTG CAC GAG AAG AAA GGG GAC GTT GCA CTG CCT    696
Pro Gln Leu Val Val Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro    138

GTC CCC TAT GAT CAC CAA CGT GGC TTT TCT GGT ATC TTT GAG GAC AGA AGC    747
Val Pro Tyr Asp His Gln Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser    155

TAC ATC TGC AAA ACC ACC ATT GGG GAC AGG GAG GTG GAT TCT GAT GCC TAC    798
Tyr Ile Cys Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr    172

TAT GTC TAC AGA CTC CAG GTG TCA TCC ATC AAC GTC TCT GTG AAC GCA GTG    849
Tyr Val Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val    189

CAG ACT GTG GTC CGC CAG GGT GAG AAC ATC ACC CTC ATG TGC ATT GTG ATC    900
Gln Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile    206

GGG AAT GAT GTG GTC AAC TTC GAG TGG ACA TAC CCC CGC AAA GAA AGT GGG    951
Gly Asn Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly    223

CGG CTG GTG GAG CCG GTG ACT GAC TTC CTC TTG GAT ATG CCT TAC CAC ATC    1002
Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile    240

CGC TCC ATC CTG CAC ATC CCC AGT GCC GAG TTA GAA GAC TCG GGG ACC TAC    1053
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                Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr Tyr   257

ACC TGC AAT GTG ACG GAG AGT GTG AAT GAC CAT CAG GAT GAA AAG GCC ATC              1104
Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys Ala Ile              274

AAC ATC ACC GTG GTT GAG AGC GGC TAC GTG CGG CTC CTG GGA GAG GTG GGC              1155
Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly Glu Val Gly              291

ACA CTA CAA TTT GCT GAG CTG CAT CGG AGC CGG ACA CTG CAG GTA GTG TTC              1206
Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu Gln Val Val Phe              308

GAG GCC TAC CCA CCG CCC ACT GTC CTG TGG TTC AAA GAC AAC CGC ACC CTG              1257
Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp Phe Lys Asp Asn Arg Thr Leu              325

GGC GAC TCC AGC GCT GGC GAA ATC GCC CTG TCC ACG CGC AAC GTG TCG GAG              1308
Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser Thr Arg Asn Val Ser Glu              342

ACC CGG TAT GTG TCA GAG CTG ACA CTG GTT CGC GTG AAG GTG GCA GAG GCT              1359
Thr Arg Tyr Val Ser Glu Leu Thr Leu Val Arg Val Lys Val Ala Glu Ala              359

GGC CAC TAC ACC ATG CGG GCC TTC CAT GAG GAT GCT GAG GTC CAG CTC TCC              1410
Gly His Tyr Thr Met Arg Ala Phe His Glu Asp Ala Glu Val Gln Leu Ser              376

TTC CAG CTA CAG ATC AAT GTC CCT GTC CGA GTG CTG GAG CTA AGT GAG AGC              1461
Phe Gln Leu Gln Ile Asn Val Pro Val Arg Val Leu Glu Leu Ser Glu Ser              393

CAC CCT GAC AGT GGG GAA CAG ACA GTC CGC TGT CGT GGC CGG GGC ATG CCG              1512
His Pro Asp Ser Gly Glu Gln Thr Val Arg Cys Arg Gly Arg Gly Met Pro              410

CAG CCG AAC ATC ATC TGG TCT GCC TGC AGA GAC CTC AAA AGG TGT CCA CGT              1563
Gln Pro Asn Ile Ile Trp Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg              427

GAG CTG CCG CCC ACG CTG CTG GGG AAC AGT TCC GAA GAG GAG AGC CAG CTG              1614
Glu Leu Pro Pro Thr Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu              444

GAG ACT AAC GTG ACG TAC TGG GAG GAG GAG CAG GAG TTT GAG GTG GTG AGC              1665
Glu Thr Asn Val Thr Tyr Trp Glu Glu Glu Gln Glu Phe Glu Val Val Ser              461

ACA CTG CGT CTG CAG CAC GTG GAT CGG CCA CTG TCG GTG CGC TGC ACG CTG              1716
Thr Leu Arg Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu              478

CGC AAC GCT GTG GGC CAG GAC ACG CAG GAG GTC ATC GTG GTG CCA CAC TCC              1767
Arg Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser              495

TTG CCC TTT AAG GTG GTG GTG ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC              1818
Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu              512

ACC ATC ATC TCC CTT ATC ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT              1869
Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg              529

TAC GAG ATC CGA TGG AAG GTG ATT GAG TCT GTG AGC TCT GAC GGC CAT GAG              1920
Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly His Glu              546

TAC ATC TAC GTG GAC CCC ATG CAG CTG CCC TAT GAC TCC ACG TGG GAG CTG              1971
Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr Trp Glu Leu              563

CCG CGG GAC CAG CTT GTG CTG GGA CGC ACC CTC GGC TCT GGG GCC TTT GGG              2022
Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser Gly Ala Phe Gly              580
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CAG GTG GTG GAG GCC ACA GCT CAT GGT CTG AGC CAT TCT CAG GCC ACG ATG   2073
Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His Ser Gln Ala Thr Met    597

AAA GTG GCC GTC AAG ATG CTT AAA TCC ACA GCC CGC AGC AGT GAG AAG CAA   2124
Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala Arg Ser Ser Glu Lys Gln    614

GCC CTT ATG TCG GAG CTG AAG ATC ATG AGT CAC CTT GGG CCC CAC CTG AAC   2175
Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu Gly Pro His Leu Asn    631

GTG GTC AAC CTG TTG GGG GCC TGC ACC AAA GGA GGA CCC ATC TAT ATC ATC   2226
Val Val Asn Leu Leu Gly Ala Cys Thr Lys Gly Gly Pro Ile Tyr Ile Ile    648

ACT GAG TAC TGC CGC TAC GGA GAC CTG GTG GAC TAC CTG CAC CGC AAC AAA   2277
Thr Glu Tyr Cys Arg Tyr Gly Asp Leu Val Asp Tyr Leu His Arg Asn Lys    665

CAC ACC TTC CTG CAG CAC CAC TCC GAC AAG CGC CGC CCG CCC AGC GCG GAG   2328
His Thr Phe Leu Gln His His Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu    682

CTC TAC AGC AAT GCT CTG CCC GTT GGG CTC CCC CTG CCC AGC CAT GTG TCC   2379
Leu Tyr Ser Asn Ala Leu Pro Val Gly Leu Pro Leu Pro Ser His Val Ser    699

TTG ACC GGG GAG AGC GAC GGT GGC TAC ATG GAC ATG AGC AAG GAC GAG TCG   2430
Leu Thr Gly Glu Ser Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser    716

GTG GAC TAT GTG CCC ATG CTG GAC ATG AAA GGA GAC GTC AAA TAT GCA GAC   2481
Val Asp Tyr Val Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp    733

ATC GAG TCC TCC AAC TAC ATG GCC CCT TAC GAT AAC TAC GTT CCC TCT GCC   2532
Ile Glu Ser Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala    750

CCT GAG AGG ACC TGC CGA GCA ACT TTG ATC AAC GAG TCT CCA GTG CTA AGC   2583
Pro Glu Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser    767

TAC ATG GAC CTC GTG GGC TTC AGC TAC CAG GTG GCC AAT GGC ATG GAG TTT   2634
Tyr Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe    784

CTG GCC TCC AAG AAC TGC GTC CAC AGA GAC CTG GCG GCT AGG AAC GTG CTC   2685
Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val Leu    801

ATC TGT GAA GGC AAG CTG GTC AAG ATC TGT GAC TTT GGC CTG GCT CGA GAC   2736
Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp    818

ATC ATG CGG GAC TCG AAT TAC ATC TCC AAA GGC AGC ACC TTT TTG CCT TTA   2787
Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe Leu Pro Leu    835

AAG TGG ATG GCT CCG GAG AGC ATC TTC AAC AGC CTC TAC ACC ACC CTG AGC   2838
Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr Thr Thr Leu Ser    852

GAC GTG TGG TCC TTC GGG ATC CTG CTC TGG GAG ATC TTC ACC TTG GGT GGC   2889
Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly    869

ACC CCT TAC CCA GAG CTG CCC ATG AAC GAG CAG TTC TAC AAT GCC ATC AAA   2940
Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln Phe Tyr Asn Ala Ile Lys    886

CGG GGT TAC CGC ATG GCC CAG CCT GCC CAT GCC TCC GAC GAG ATC TAT GAG   2991
Arg Gly Tyr Arg Met Ala Gln Pro Ala His Ala Ser Asp Glu Ile Tyr Glu    903
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ATC ATG CAG AAG TGC TGG GAA GAG AAG TTT GAG ATT CGG CCC CCC TTC TCC   3042
Ile Met Gln Lys Cys Trp Glu Glu Lys Phe Glu Ile Arg Pro Pro Phe Ser    920

CAG CTG GTG CTG CTT CTC GAG AGA CTG TTG GGC GAA GGT TAC AAA AAG AAG   3093
Gln Leu Val Leu Leu Leu Glu Arg Leu Leu Gly Glu Gly Tyr Lys Lys Lys    937

TAC CAG CAG GTG GAT GAG GAG TTT CTG AGG AGT GAC CAC CCA GCC ATC CTT   3144
Tyr Gln Gln Val Asp Glu Glu Phe Leu Arg Ser Asp His Pro Ala Ile Leu    954

CGG TCC CAG GCC CGC TTG CCT GGG TTC CAT GGC CTC CGA TCT CCC CTG GAC   3195
Arg Ser Gln Ala Arg Leu Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp    971

ACC AGC TCC GTC CTC TAT ACT GCC GTG CAG CCC AAT GAG GGT GAC AAC GAC   3246
Thr Ser Ser Val Leu Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp    988

TAT ATC ATC CCC CTG CCT GAC CCC AAA CCT GAG GTT GCT GAC GAG GGC CCA   3297
Tyr Ile Ile Pro Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro   1005

CTG GAG GGT TCC CCC AGC CTA GCC AGC TCC ACC CTG AAT GAA GTC AAC ACC   3348
Leu Glu Gly Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr   1022

TCC TCA ACC ATC TCC TGT GAC AGC CCC CTG GAG CCC CAG GAC GAA CCA GAG   3399
Ser Ser Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu   1039

CCA GAG CCC CAG CTT GAG CTC CAG GTG GAG CCG GAG CCG GAG CTG GAA CAG   3450
Pro Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln   1056

TTG CCG GAT TCG GGG TGC CCT GCG CCT CGG GCG GAA GCA GAG GAT AGC TTC   3501
Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser Phe   1073

CTG TAGGGGGCTGGCCCCTACCCTGCCCTGCCTGAAGCTCCCCCGCTGCCAGCACCCAGCATCTCC   3567
Leu                                                                     1074

TGGCCTGGCCTGGCCGGGCTTCCTGTCAGCCAGGCTGCCCTTATCAGCTGTCCCCTTCTGGAAGCTT   3634

TCTGCTCCTGACGTGTTGTGCCCCAAACCCTGGGGCTGGCTTAGGAGGCAAGAAAACTGCAGGGGCC   3701

GTGACCAGCCCTCTGCCTCCAGGGAGGCCAACTGACTCTGAGCCAGGGTTCCCCCAGGGAACTCAGT   3768

TTTCCCATATGTAAGATGGGAAAGTTAGGCTTGATGACCCAGAATCTAGGATTCTCTCCCTGGCTGA   3835

CAGGTGGGGAGACCGAATCCCTCCCTGGGAAGATTCTTGGAGTTACTGAGGTGGTAAATTAACTTTT   3902

TTCTGTTCAGCCAGCTACCCCTCAAGGAATCATAGCTCTCTCCTCGCACTTTTATCCACCCAGGAGC   3969

TAGGGAAGAGACCCTAGCCTCCCTGGCTGCTGGCTGAGCTAGGGCCTAGCCTTGAGCAGTGTTGCCT   4036

CATCCAGAAGAAAGCCAGTCTCCTCCCTATGATGCCAGTCCCTGCGTTCCCTGGCCCGAGCTGGTCT   4103

GGGGCCATTAGGCAGCCTAATTAATGCTGGAGGCTGAGCCAAGTACAGGACACCCCCAGCCTGCAGC   4170

CCTTGCCCAGGGCACTTGGAGCACACGCAGCCATAGCAAGTGCCTGTGTCCCTGTCCTTCAGGCCCA   4237

TCAGTCCTGGGGCTTTTTCTTTATCACCCTCAGTCTTAATCCATCCACCAGAGTCTAGAAGGCCAGA   4304

CGGGCCCCGCATCTGTGATGAGAATGTAAATGTGCCAGTGTGGAGTGGCCACGTGTGTGTGCCAGAT   4371

ATGGCCCTGGCTCTGCATTGGACCTGCTATGAGGCTTTGGAGGAATCCCTCACCCTCTCTGGGCCTC   4438
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AGTTTCCCCTTCAAAAAATGAATAAGTCGGACTTATTAACTCTGAGTGCCTTGCCAGCACTAACATT   4505

CTAGAGTATCCAGGTGGTTGCACATTTGTCCAGATGAAGCAAGGCCATATACCCTAAACTTCCATCC   4572

TGGGGGTCAGCTGGGCTCCTGGGAGATTCCAGATCACACATCACACTCTGGGGACTCAGGAACCATG   4639

CCCCTTCCCCAGGCCCCCAGCAAGTCTCAAGAACACAGCTGCACAGGCCTTGACTTAGAGTGACAGC   4706

CGGTGTCCTGGAAAGCCCCGCAGCAGCTGCCCCAGGGACATGGGAAGACCACGGGACCTCTTTCACTA   4773

CCCACGATGACCTCCGGGGGTATCCTGGGCAAAAGGGACAAAGAGGGCAAATGAGATCACCTCCTGC   4840

AGCCCACCACTCCAGCACCTGTGCCGAGGTCTGCGTCGAAGACAGAATGGACAGTGAGGACAGTTAT   4907

GTCTTGTAAAAGACAAGAAGCTTCAGATGGGTACCCCAAGAAGGATGTGAGAGGTGGGCGCTTTGGA   4974

GGTTTGCCCCTCACCCACCAGCTGCCCCATCCCTGAGGCAGCGCTCCATGGGGGTATGGTTTTGTCA   5041

CTGCCCAGACCTAGCAGTGACATCTCATTGTCCCCAGCCCAGTGGGCATTGGAGGTGCCAGGGGAGT   5108

CAGGGTTGTAGCCAAGACGCCCCCGCACGGGGAGGGTTGGGAAGGGGGTGCAGGAAGCTCAACCCCT   5175

CTGGGCACCAACCCTGCATTGCAGGTTGGCACCTTACTTCCCTGGGATCCCAGAGTTGGTCCAAGGA   5242

GGGAGAGTGGGTTCTCAATACGGTACCAAAGATATAATCACCTAGGTTTACAAATATTTTTAGGACT   5309

CACGTTAACTCACATTTATACAGCAGAAATGCTATTTTGTATGCTGTTAAGTTTTTCTATCTGTGTA   5376

CTTTTTTTTAAGGGAAAGATTTTAATATTAAACCTGGTGCTTCTCACTCAC               5427
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Sequence of human PDGF receptor alpha   Genbank Accession # M22734

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                TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGGAGGCCGTGGGC      61

ACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCT         128

ATG GGG ACT TCC CAT CCG GCG TTC CTG GTC TTA GGC TGT CTT CTC ACA GGG         179
Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu Leu Thr Gly          -7

CTG AGC CTA ATC CTC TGC CAG CTT TCA TTA CCC TCT ATC CTT CCA AAT GAA         230
Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile Leu Pro Asn Glu          11

AAT GAA AAG GTT GTG CAG CTG AAT TCA TCC TTT TCT CTG AGA TGC TTT GGG         281
Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser Leu Arg Cys Phe Gly          28

GAG AGT GAA GTG AGC TGG CAG TAC CCC ATG TCT GAA GAA GAG AGC TCC GAT         332
Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser Glu Glu Glu Ser Ser Asp          45

GTG GAA ATC AGA AAT GAA GAA AAC AAC AGC GGC CTT TTT GTG ACG GTC TTG         383
Val Glu Ile Arg Asn Glu Glu Asn Asn Ser Gly Leu Phe Val Thr Val Leu          62

GAA GTG AGC AGT GCC TCG GCG GCC CAC ACA GGG TTG TAC ACT TGC TAT TAC         434
Glu Val Ser Ser Ala Ser Ala Ala His Thr Gly Leu Tyr Thr Cys Tyr Tyr          79

AAC CAC ACT CAG ACA GAA GAG AAT GAG CTT GAA GGC AGG CAC ATT TAC ATC         485
Asn His Thr Gln Thr Glu Glu Asn Glu Leu Glu Gly Arg His Ile Tyr Ile          96

TAT GTG CCA GAC CCA GAT GTA GCC TTT GTA CCT CTA GGA ATG ACG GAT TAT         536
Tyr Val Pro Asp Pro Asp Val Ala Phe Val Pro Leu Gly Met Thr Asp Tyr         113

TTA GTC ATC GTG GAG GAT GAT GAT TCT GCC ATT ATA CCT TGT CGC ACA ACT         587
Leu Val Ile Val Glu Asp Asp Asp Ser Ala Ile Ile Pro Cys Arg Thr Thr         130

GAT CCC GAG ACT CCT GTA ACC TTA CAC AAC AGT GAG GGG GTG GTA CCT GCC         638
Asp Pro Glu Thr Pro Val Thr Leu His Asn Ser Glu Gly Val Val Pro Ala         147

TCC TAC GAC AGC AGA CAG GGC TTT AAT GGG ACC TTC ACT GTA GGG CCC TAT         689
Ser Tyr Asp Ser Arg Gln Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr         164

ATC TGT GAG GCC ACC GTC AAA GGA AAG AAG TTC CAG ACC ATC CCA TTT AAT         740
Ile Cys Glu Ala Thr Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn         181

GTT TAT GCT TTA AAA GCA ACA TCA GAG CTG GAT CTA GAA ATG GAA GCT CTT         791
Val Tyr Ala Leu Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu         198

AAA ACC GTG TAT AAG TCA GGG GAA ACG ATT GTG GTC ACC TGT GCT GTT TTT         842
Lys Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe         215

AAC AAT GAG GTG GTT GAC CTT CAA TGG ACT TAC CCT GGA GAA GTG AAA GGC         893
Asn Asn Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly         232

AAA GGC ATC ACA ATG CTG GAA GAA ATC AAA GTC CCA TCC ATC AAA TTG GTG         944
Lys Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val         249

TAC ACT TTG ACG GTC CCC GAG GCC ACG GTG AAA GAC AGT GGA GAT TAC GAA         995
Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr Glu         266
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TGT GCT GCC CGC CAG GCT ACC AGG GAG GTC AAA GAA ATG AAG AAA GTC ACT   1046
Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys Val Thr    283

ATT TCT GTC CAT GAG AAA GGT TTC ATT GAA ATC AAA CCC ACC TTC AGC CAG   1097
Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr Phe Ser Gln    300

TTG GAA GCT GTC AAC CTG CAT GAA GTC AAA CAT TTT GTT GTA GAG GTG CGG   1148
Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val Val Glu Val Arg    317

GCC TAC CCA CCT CCC AGG ATA TCC TGG CTG AAA AAC AAT CTG ACT CTG ATT   1199
Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn Asn Leu Thr Leu Ile    334

GAA AAT CTC ACT GAG ATC ACC ACT GAT GTG GAA AAG ATT CAG GAA ATA AGG   1250
Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu Lys Ile Gln Glu Ile Arg    351

TAT CGA AGC AAA TTA AAG CTG ATC CGT GCT AAG GAA GAA GAC AGT GGC CAT   1301
Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala Lys Glu Glu Asp Ser Gly His    368

TAT ACT ATT GTA GCT CAA AAT GAA GAT GCT GTG AAG AGC TAT ACT TTT GAA   1352
Tyr Thr Ile Val Ala Gln Asn Glu Asp Ala Val Lys Ser Tyr Thr Phe Glu    385

CTG TTA ACT CAA GTT CCT TCA TCC ATT CTG GAC TTG GTC GAT GAT CAC CAT   1403
Leu Leu Thr Gln Val Pro Ser Ser Ile Leu Asp Leu Val Asp Asp His His    402

GGC TCA ACT GGG GGA CAG ACG GTG AGG TGC ACA GCT GAA GGC ACG CCG CTT   1454
Gly Ser Thr Gly Gly Gln Thr Val Arg Cys Thr Ala Glu Gly Thr Pro Leu    419

CCT GAT ATT GAG TGG ATG ATA TGC AAA GAT ATT AAG AAA TGT AAT AAT GAA   1505
Pro Asp Ile Glu Trp Met Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu    436

ACT TCC TGG ACT ATT TTG GCC AAC AAT GTC TCA AAC ATC ATC ACG GAG ATC   1556
Thr Ser Trp Thr Ile Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile    453

CAC TCC CGA GAC AGG AGT ACC GTG GAG GGC CGT GTG ACT TTC GCC AAA GTG   1607
His Ser Arg Asp Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val    470

GAG GAG ACC ATC GCC GTG CGA TGC CTG GCT AAG AAT CTC CTT GGA GCT GAG   1658
Glu Glu Thr Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu    487

AAC CGA GAG CTG AAG CTG GTG GCT CCC ACC CTG CGT TCT GAA CTC ACG GTG   1709
Asn Arg Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val    504

GCT GCT GCA GTC CTG GTG CTG TTG GTG ATT GTG ATC ATC TCA CTT ATT GTC   1760
Ala Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val    521

CTG GTT GTC ATT TGG AAA CAG AAA CCG AGG TAT GAA ATT CGC TGG AGG GTC   1811
Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg Val    538

ATT GAA TCA ATC AGC CCA GAT GGA CAT GAA TAT ATT TAT GTG GAC CCG ATG   1862
Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp Pro Met    555

CAG CTG CCT TAT GAC TCA AGA TGG GAG TTT CCA AGA GAT GGA CTA GTG CTT   1913
Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly Leu Val Leu    572

GGT CGG GTC TTG GGG TCT GGA GCG TTT GGG AAG GTG GTT GAA GGA ACA GCC   1964
Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val Glu Gly Thr Ala    589
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TAT GGA TTA AGC CGG TCC CAA CCT GTC ATG AAA GTT GCA GTG AAG ATG CTA   2015
Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val Ala Val Lys Met Leu    606

AAA CCC ACG GCC AGA TCC AGT GAA AAA CAA GCT CTC ATG TCT GAA CTG AAG   2066
Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys   623

ATA ATG ACT CAC CTG GGG CCA CAT TTG AAC ATT GTA AAC TTG CTG GGA GCC   2117
Ile Met Thr His Leu Gly Pro His Leu Asn Ile Val Asn Leu Leu Gly Ala   640

TGC ACC AAG TCA GGC CCC ATT TAC ATC ATC ACA GAG TAT TGC TTC TAT GGA   2168
Cys Thr Lys Ser Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Phe Tyr Gly   657

GAT TTG GTC AAC TAT TTG CAT AAG AAT AGG'GAT AGC TTC CTG AGC CAC CAC   2219
Asp Leu Val Asn Tyr Leu His Lys Asn Arg Asp Ser Phe Leu Ser His His   674

CCA GAG AAG CCA AAG AAA GAG CTG GAT ATC TTT GGA TTG AAC CCT GCT GAT   2270
Pro Glu Lys Pro Lys Lys Glu Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp   691

GAA AGC ACA CGG AGC TAT GTT ATT TTA TCT TTT GAA AAC AAT GGT GAC TAC   2321
Glu Ser Thr Arg Ser Tyr Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr   708

ATG GAC ATG AAG CAG GCT GAT ACT ACA CAG TAT GTC CCC ATG CTA GAA AGG   2372
Met Asp Met Lys Gln Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg   725

AAA GAG GTT TCT AAA TAT TCC GAC ATC CAG AGA TCA CTC TAT GAT CGT CCA   2423
Lys Glu Val Ser Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro   742

GCC TCA TAT AAG AAG AAA TCT ATG TTA GAC TCA GAA GTC AAA AAC CTC CTT   2474
Ala Ser Tyr Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu   759

TCA GAT GAT AAC TCA GAA GGC CTT ACT TTA TTG GAT TTG TTG AGC TTC ACC   2525
Ser Asp Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Phe Thr   776

TAT CAA GTT GCC CGA GGA ATG GAG TTT TTG GCT TCA AAA AAT TGT GTC CAC   2576
Tyr Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His   793

CGT GAT CTG GCT GCT CGC AAC GTT CTC CTG GCA CAA GGA AAA ATT GTG AAG   2627
Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val Lys   810

ATC TGT GAC TTT GGC CTG GCC AGA GAC ATC ATG CAT GAT TCG AAC TAT GTG   2678
Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn Tyr Val   827

TCG AAA GGC AGT ACC TTT CTG CCC GTG AAG TGG ATG GCT CCT GAG AGC ATC   2729
Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile   844

TTT GAC AAC CTC TAC ACC ACA CTG AGT GAT GTC TGG TCT TAT GGC ATT CTG   2780
Phe Asp Asn Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser Tyr Gly Ile Leu   861

CTC TGG GAG ATC TTT TCC CTT GGT GGC ACC CCT TAC CCC GGC ATG ATG GTG   2831
Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr Pro Gly Met Met Val   878

GAT TCT ACT TTC TAC AAT AAG ATC AAG AGT GGG TAC CGG ATG GCC AAG CCT   2882
Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly Tyr Arg Met Ala Lys Pro   895

GAC CAC GCT ACC AGT GAA GTC TAC GAG ATC ATG GTG AAA TGC TGG AAC AGT   2933
Asp His Ala Thr Ser Glu Val Tyr Glu Ile Met Val Lys Cys Trp Asn Ser   912
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GAG CCG GAG AAG AGA CCC TCC TTT TAC CAC CTG AGT GAG ATT GTG GAG AAT   2984
Glu Pro Glu Lys Arg Pro Ser Phe Tyr His Leu Ser Glu Ile Val Glu Asn    929

CTG CTG CCT GGA CAA TAT AAA AAG AGT TAT GAA AAA ATT CAC CTG GAC TTC   3035
Leu Leu Pro Gly Gln Tyr Lys Lys Ser Tyr Glu Lys Ile His Leu Asp Phe    946

CTG AAG AGT GAC CAT CCT GCT GTG GCA CGC ATG CGT GTG GAC TCA GAC AAT   3086
Leu Lys Ser Asp His Pro Ala Val Ala Arg Met Arg Val Asp Ser Asp Asn    963

GCA TAC ATT GGT GTC ACC TAC AAA AAC GAG GAA GAC AAG CTG AAG GAC TGG   3137
Ala Tyr Ile Gly Val Thr Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp    980

GAG GGT GGT CTG GAT GAG CAG AGA CTG AGC GCT GAC AGT GGC TAC ATC ATT   3188
Glu Gly Gly Leu Asp Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile    997

CCT CTG CCT GAC ATT GAC CCT GTC CCT GAG GAG GAG GAC CTG GGC AAG AGG   3239
Pro Leu Pro Asp Ile Asp Pro Val Pro Glu Glu Glu Asp Leu Gly Lys Arg   1014

AAC AGA CAC AGC TCG CAG ACC TCT GAA GAG AGT GCC ATT GAG ACG GGT TCC   3290
Asn Arg His Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser   1031

AGC AGT TCC ACC TTC ATC AAG AGA GAG GAC GAG ACC ATT GAA GAC ATC GAC   3341
Ser Ser Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp   1048

ATG ATG GAC GAC ATC GGC ATA GAC TCT TCA GAC CTG GTG GAA GAC AGC TTC   3392
Met Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe   1065

CTG   TAACTGGCGGATTCGAGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAA   3458
Leu                                                                     1066

CCACTTTATTGCAATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCA   3525

AGGGCCTCGGGGAGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTG   3592

CCTCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATA   3659

ATAGGCCACAGAAGGTGAACTTTCTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATA   3726

CTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCTGTGTTTAGATTGTATT   3793

AACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCTCTTGAAACCTGA   3860

TGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTTTGACCTTAAAAGGTACTGG   3927

TACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTT   3994

TAATAGATTTGGGTCATTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACT   4061

ACTACTGTTATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCACACAAAGCACAAT   4128

TTAAAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATG   4195

TTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAA   4262

AGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTAA   4329

AAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCCTAAAAGTT   4396
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